

Karaolis1.ST25.txt
SEQUENCE LISTING

<110> KARAOLIS, David K.R.

<120> METHOD FOR ATTENUATING VIRULENCE OF MICROBIAL PATHOGENS AND FOR INHIBITING MICROBIAL BIOFILM FORMATION

<130> KARAOLIS1 PCT

<140> NOT YET ASSIGNED

<141> 2004-07-22

<150> 60/490,029

<151> 2003-07-25

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 2055

<212> DNA

<213> V. cholerae

<220>

<221> CDS

<222> (1)..(2055)

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acg tca cac agt ccg ttc ttt ttt gca atc ctc aat gat caa cac caa	96
Thr Ser His Ser Pro Phe Phe Phe Ala Ile Leu Asn Asp Gln His Gln	
20 25 30	
tac gtg atg gtc aac gag cgc tat tgt gat atc gcc ggt ctc tct agc	144
Tyr Val Met Val Asn Glu Arg Tyr Cys Asp Ile Ala Gly Leu Ser Ser	
35 40 45	
gaa gag atg gtc ggg atg agc gat agt cag gtt ctg ggc gaa cat ttt	192
Glu Glu Met Val Gly Met Ser Asp Ser Gln Val Leu Gly Glu His Phe	
50 55 60	
tat cgc cat ctc aaa ccg ttt tac gaa cgt gcg ttt aac aac gag cat	240
Tyr Arg His Leu Lys Pro Phe Tyr Glu Arg Ala Phe Asn Asn Glu His	
65 70 75 80	
att gag tcc gag ctg acc ctc agc gaa atc gac ctc gaa acc agc tta	288
Ile Glu Ser Glu Leu Thr Leu Ser Glu Ile Asp Leu Glu Thr Ser Leu	
85 90 95	
cac ttt tct ctc tcc ccc atc atg atc aac gat cgg gtg caa tac ctt	336
His Phe Ser Leu Ser Pro Ile Met Ile Asn Asp Arg Val Gln Tyr Leu	
100 105 110	
gta ttc cac gcg att gat acc tca gaa aag cag att tta gtg cgc tct	384
Val Phe His Ala Ile Asp Thr Ser Glu Lys Gln Ile Leu Val Arg Ser	
115 120 125	
ctg gaa gaa tcg gaa agc aaa tac gca ctc ctc acg aca ctg cta cct	432
Leu Glu Glu Ser Glu Ser Lys Tyr Ala Leu Leu Thr Thr Leu Leu Pro	
130 135 140	
gat ggt tta atg atg gtg gaa aat gac tgc att att tct gcc aac cct	480
Asp Gly Leu Met Met Val Glu Asn Asp Cys Ile Ile Ser Ala Asn Pro	

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145	150	155	160	
tcc gct gca cgt tta ctc ggt ttt gac gac gca caa aaa ctg ctc gga Ser Ala Ala Arg Leu Leu Gly Phe Asp Asp Ala Gln Lys Leu Leu Gly	165	170	175	528
gaa aat ctc tcc aga ctg ttt att gat gaa aag acc aaa acc gtt ttt Glu Asn Leu Ser Arg Leu Phe Ile Asp Glu Lys Thr Lys Thr Val Phe	180	185	190	576
tca tcg cag ttg gct tcg cta ctg aca gaa aaa ccc ttg gtg tgc ttg Ser Ser Gln Leu Ala Ser Leu Leu Thr Glu Lys Pro Leu Val Cys Leu	195	200	205	624
acc ggg cca agg tgt ggg ttt gaa cgg aaa atc cag tta cac gca ggt Thr Gly Pro Arg Cys Gly Phe Glu Arg Lys Ile Gln Leu His Ala Gly	210	215	220	672
tgc acc tct tta ctc ggt aat cag tcg cag ttg atc tta ttg caa gat Cys Thr Ser Leu Leu Gly Asn Gln Ser Gln Leu Ile Leu Leu Gln Asp	225	230	235	720
gcc gat gaa gcc cca aaa cag ttt tct gcg acc act caa gtc gat gcg Ala Asp Glu Ala Pro Lys Gln Phe Ser Ala Thr Thr Gln Val Asp Ala	245	250	255	768
cat att gat agc ctc act ggg ctg tat aac cga cac ggg ttt acc aag His Ile Asp Ser Leu Thr Gly Leu Tyr Asn Arg His Gly Phe Thr Lys	260	265	270	816
cgc tta gag cag tgc atc caa aat gag acg cct ttg gtt atg ctc tat Arg Leu Glu Gln Cys Ile Gln Asn Glu Thr Pro Leu Val Met Leu Tyr	275	280	285	864
ctg gac att gat aac ttc aaa aac atc aat gac tct ctc ggc cat cac Leu Asp Ile Asp Asn Phe Lys Asn Ile Asn Asp Ser Leu Gly His His	290	295	300	912
atc ggt gac aaa gtg att aaa gag gtg gcg gca cgt tta aaa cgc tta Ile Gly Asp Lys Val Ile Lys Glu Val Ala Ala Arg Leu Lys Arg Leu	305	310	315	960
ctg cca cag caa gcc gta ctt ggc cat ttg ggc ggt gat gag ttt ggt Leu Pro Gln Gln Ala Val Leu Gly His Leu Gly Gly Asp Glu Phe Gly	325	330	335	1008
ttg atc ttg ccg gag cca gaa cac aac cgc tct gca gaa atg ttg gca Leu Ile Leu Pro Glu Pro Glu His Asn Arg Ser Ala Glu Met Leu Ala	340	345	350	1056
gat cgc att atc tct ttg att aat cag cct ttt gac ctg cac cat ttc Asp Arg Ile Ile Ser Leu Ile Asn Gln Pro Phe Asp Leu His His Phe	355	360	365	1104
agt aag cgt tta gct tgt tcg att ggc agc gtg cgt tat ccc ggt gac Ser Lys Arg Leu Ala Cys Ser Ile Gly Ser Val Arg Tyr Pro Gly Asp	370	375	380	1152
ggc aat gat gct cgc gta tta ctg caa aat gcc gat acc gcg atg tat Gly Asn Asp Ala Arg Val Leu Leu Gln Asn Ala Asp Thr Ala Met Tyr	385	390	395	1200
gag gct aaa gag cgc ggt cgc aat cgc ctg atc aaa ttc aat gat cag Glu Ala Lys Glu Arg Gly Arg Asn Arg Leu Ile Lys Phe Asn Asp Gln	405	410	415	1248
atg aac aaa gaa gcg cgg atg cgc ctt tgg ttg gaa att gaa ctg caa Met Asn Lys Glu Ala Arg Met Arg Leu Trp Leu Glu Ile Glu Leu Gln				1296

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420								425		430					
aaa gcg cta caa caa aac ggc cta gaa gtg tgg tac caa ccg aaa gtc	Lys Ala Leu 435	Gln Gln Asn Gly	Leu 440	Glu Val Trp Tyr	Gln 445	Pro Lys Val									1344
aac gcg cgt gat ttt agc atc aat ggc gca gaa gcc ttg gta cgc tgg	Asn Ala 450	Arg Asp Phe Ser	Ile 455	Asn Gly Ala Glu Ala 460	Leu Val Arg Trp										1392
aaa cat ccc gtt gaa ggc tat atc agc cca ggt gct ttc att ccc gtt	Lys His Pro Val 465	Glu Gly Tyr Ile Ser Pro	Gly 470	Gly Ala Phe Ile Pro	Val 480										1440
gcg gaa aaa gcc ggc tta atc gaa cat ttg ggt cgc gtg gtt atg cgt	Ala Glu Lys Ala 485	Gly Leu Ile Glu His	Leu 490	Arg Val Val Met 495	Arg										1488
gaa gtc ttc gcg acc gtc aag cgc tgg aag cta caa ggc att tta ccc	Glu Val Phe Ala 500	Thr Val Lys Arg Trp 505	Lys	Gln Gly Ile Leu Pro											1536
gga cgt gtg gcg atc aac atc tcc ccc gag cag ttt ggc aat cct caa	Gly Arg Val 515	Ala Ile Asn Ile Ser 520	Pro	Glu Gln Phe Gly 525	Asn Pro Gln										1584
ctg att gat tat tta gaa aaa cta ctg cga aca act ggg cta gat ccc	Leu Ile Asp Tyr Leu 530	Glu Lys 535	Leu Leu Arg Thr 540	Gly Leu Asp Pro											1632
aac aac atc aca ttt gaa ctg acc gaa agt gtg gtg atg agc gat agt	Asn Asn Ile Thr Phe 545	Glu Leu Thr Glu Ser 555	Val Val Met Ser Asp Ser 560												1680
gaa cat acc cag caa atg ctc aat gcc atc aag aaa ctc ggc ttc acc	Glu His Thr Gln 565	Met Leu Asn Ala Ile 570	Lys Lys Leu Gly Phe 575	Thr											1728
ttg tca att gat gac ttc ggt aca ggt tac tgc tgc ctg gct tat tta	Leu Ser Ile Asp 580	Phe Gly Thr 585	Tyr Ser Ser Leu 590	Tyr Leu											1776
gct cgc ttc ccg atc gat gag ctc aaa atc gac cgc gcg ttt atc agt	Ala Arg Phe 595	Pro Ile Asp Glu Leu 600	Lys Ile Asp Arg Ala Phe 605	Ile Ser											1824
aat atc gac act cta ccc aaa cag ctc acg gtg att gaa aac atc att	Asn Ile Asp Thr Leu 610	Pro Lys 615	Gln Leu Thr Val Ile 620	Glu Asn Ile Ile											1872
aat ttg ggg cgc tca ctg aac ctg acc gta gtt gca gaa gga gta gaa	Asn Leu Gly Arg Ser 625	Leu Asn Leu Thr Val 635	Ala Glu Gly Val 640												1920
act cag caa caa gcc act tta ctc tcc aac cta aat tgc cac tcc atc	Thr Gln Gln Gln 645	Thr Leu Leu Ser Asn 650	Leu Asn Cys His Ser 655	Ile											1968
caa ggc ttc cat ttt tat cgc cca caa ccg aag cac gaa gtg gaa gag	Gln Gly Phe His Phe Tyr Arg Pro 665	Gln Pro Lys His Glu Val 670	Glu Glu												2016
ttg ttt gcg caa aat cgc cgc cat cgc aaa tcc ctc taa	Leu Phe Ala Gln Asn Arg Arg His 680	Lys Ser Leu													2055

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<211> 684

<212> PRT

<213> V. cholerae

<400> 2

Met Pro Ala Gln Thr Ser Ser Gln Leu Lys His Trp Phe Ala Lys Ile
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 Tyr Val Met Val Asn Glu Arg Tyr Cys Asp Ile Ala Gly Leu Ser Ser
 35 40 45
 Glu Glu Met Val Gly Met Ser Asp Ser Gln Val Leu Gly Glu His Phe
 50 55 60
 Tyr Arg His Leu Lys Pro Phe Tyr Glu Arg Ala Phe Asn Asn Glu His
 65 70 75 80
 Ile Glu Ser Glu Leu Thr Leu Ser Glu Ile Asp Leu Glu Thr Ser Leu
 85 90 95
 His Phe Ser Leu Ser Pro Ile Met Ile Asn Asp Arg Val Gln Tyr Leu
 100 105 110
 Val Phe His Ala Ile Asp Thr Ser Glu Lys Gln Ile Leu Val Arg Ser
 115 120 125
 Leu Glu Glu Ser Glu Ser Lys Tyr Ala Leu Leu Thr Thr Leu Leu Pro
 130 135 140
 Asp Gly Leu Met Met Val Glu Asn Asp Cys Ile Ile Ser Ala Asn Pro
 145 150 155 160
 Ser Ala Ala Arg Leu Leu Gly Phe Asp Asp Ala Gln Lys Leu Leu Gly
 165 170 175
 Glu Asn Leu Ser Arg Leu Phe Ile Asp Glu Lys Thr Lys Thr Val Phe
 180 185 190
 Ser Ser Gln Leu Ala Ser Leu Leu Thr Glu Lys Pro Leu Val Cys Leu
 195 200 205
 Thr Gly Pro Arg Cys Gly Phe Glu Arg Lys Ile Gln Leu His Ala Gly
 210 215 220
 Cys Thr Ser Leu Leu Gly Asn Gln Ser Gln Leu Ile Leu Leu Gln Asp
 225 230 235 240
 Ala Asp Glu Ala Pro Lys Gln Phe Ser Ala Thr Thr Gln Val Asp Ala
 245 250 255

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His Ile Asp Ser Leu Thr Gly Leu Tyr Asn Arg His Gly Phe Thr Lys
 260 265 270
 Arg Leu Glu Gln Cys Ile Gln Asn Glu Thr Pro Leu Val Met Leu Tyr
 275 280 285
 Leu Asp Ile Asp Asn Phe Lys Asn Ile Asn Asp Ser Leu Gly His His
 290 295 300
 Ile Gly Asp Lys Val Ile Lys Glu Val Ala Ala Arg Leu Lys Arg Leu
 305 310 315 320
 Leu Pro Gln Gln Ala Val Leu Gly His Leu Gly Gly Asp Glu Phe Gly
 325 330 335
 Leu Ile Leu Pro Glu Pro Glu His Asn Arg Ser Ala Glu Met Leu Ala
 340 345 350
 Asp Arg Ile Ile Ser Leu Ile Asn Gln Pro Phe Asp Leu His His Phe
 355 360 365
 Ser Lys Arg Leu Ala Cys Ser Ile Gly Ser Val Arg Tyr Pro Gly Asp
 370 375 380
 Gly Asn Asp Ala Arg Val Leu Leu Gln Asn Ala Asp Thr Ala Met Tyr
 385 390 395 400
 Glu Ala Lys Glu Arg Gly Arg Asn Arg Leu Ile Lys Phe Asn Asp Gln
 405 410 415
 Met Asn Lys Glu Ala Arg Met Arg Leu Trp Leu Glu Ile Glu Leu Gln
 420 425 430
 Lys Ala Leu Gln Gln Asn Gly Leu Glu Val Trp Tyr Gln Pro Lys Val
 435 440 445
 Asn Ala Arg Asp Phe Ser Ile Asn Gly Ala Glu Ala Leu Val Arg Trp
 450 455 460
 Lys His Pro Val Glu Gly Tyr Ile Ser Pro Gly Ala Phe Ile Pro Val
 465 470 475 480
 Ala Glu Lys Ala Gly Leu Ile Glu His Leu Gly Arg Val Val Met Arg
 485 490 495
 Glu Val Phe Ala Thr Val Lys Arg Trp Lys Leu Gln Gly Ile Leu Pro
 500 505 510
 Gly Arg Val Ala Ile Asn Ile Ser Pro Glu Gln Phe Gly Asn Pro Gln
 515 520 525

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Leu Ile Asp Tyr Leu Glu Lys Leu Leu Arg Thr Thr Gly Leu Asp Pro
 530 535 540
 Asn Asn Ile Thr Phe Glu Leu Thr Glu Ser Val Val Met Ser Asp Ser
 545 550 555 560
 Glu His Thr Gln Gln Met Leu Asn Ala Ile Lys Lys Leu Gly Phe Thr
 565 570 575
 Leu Ser Ile Asp Asp Phe Gly Thr Gly Tyr Ser Ser Leu Ala Tyr Leu
 580 585 590
 Ala Arg Phe Pro Ile Asp Glu Leu Lys Ile Asp Arg Ala Phe Ile Ser
 595 600 605
 Asn Ile Asp Thr Leu Pro Lys Gln Leu Thr Val Ile Glu Asn Ile Ile
 610 615 620
 Asn Leu Gly Arg Ser Leu Asn Leu Thr Val Val Ala Glu Gly Val Glu
 625 630 635 640
 Thr Gln Gln Gln Ala Thr Leu Leu Ser Asn Leu Asn Cys His Ser Ile
 645 650 655
 Gln Gly Phe His Phe Tyr Arg Pro Gln Pro Lys His Glu Val Glu Glu
 660 665 670
 Leu Phe Ala Gln Asn Arg Arg His Arg Lys Ser Leu
 675 680

<210> 3
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<220>
 <223> synthetic

<400> 3
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31

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic

<400> 4
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29

<210> 5
 <211> 5

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<212> PRT
<213> Artificial

<220>
<223> synthetic

<220>
<221> misc_feature
<222> (3)..(3)
<223> Residue at this position can be either Asp or Glu.

<400> 5

Gly Gly Xaa Glu Phe
1 5